AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph at page 29, lines 1-9 with the paragraph as marked below:

Degenerate PCR primers were designed to span moderate to highly conserved regions of the eukaryotic initiation factor 1A (eIF1A) gene and the alpha-tubulin genes, based on alignments of multiple sequences of invertebrate's genes derived from GenBank. Sequences were aligned and multiple sequence comparisons were generated using either the GCG program `Pileup` or `CLUSTAL W` with default parameters for the nucleotide sequences and the default-scoring matrix for proteins. Primers were designed to cover a single putative exon whenever possible. Exon predictions were usually based on exon boundaries found in the Drosophila melanogaster orthologue of the target gene. To assist with the design process, the CODEHOP program (Blocks Server, ~~http://~~www.blocks.fhcrc.org) was used.

Please replace the paragraph at page 39, lines 28-29 with the paragraph as marked below:

Pandolfini et al. (2003) BioMedCentral (BMC) Biotechnology 3:7 (~~http://~~www.biomedcentral.com/1472-6750/3/7)